

Figure 1A

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| 1 | CCCACGCGTCCGGGGAGCTTGCACTAACATCTACAATGGCTTCTAAAAAGCACAGATGAC | 60 |
| 61 | CTGCTACACTTCCTGACTTGCTTGCTATTGGTTGGCACTGTTCATAAATATAATTTGCTC | 120 |
| 121 | TTTCACTTTTCTTTGAAATGAGCAACCTGAATTACTCGGAGGAGAAAGGCAGGAGAGATA | 180 |
| 181 | GAGGCAGCAGAAGCCAGGGCAGCTGAAAGACAGAGACCTTCAGTCTGAACCAACAACAAG | 240 |
| 241 | CAAAGTTAAATTATGGATATCCAAGGGAGTCTATAGAAGGTCCATGCAAGACATTTTGAC | 300 |
| 301 | TACTTGTCTGAACTAGATATCCCTTGAATGTGCACACAAAAAGTGAATGGGTCATTTGAT | 360 |
| 361 | AAGGGAAAACTAGGTTCCAAGATGGCTGAATAGGAAGAGCTCCAGTCTGCAGATCCCAGT | 420 |
| 421 | GTGAGCAACGTGGAAGATGGGTGATTTCTGCATTTCCAAGTGGAGAGAGAAAAATT | 480 |
| 481 | TATGTCCTTGCAACCATCCATCTCCGTATCAGAAATGGAACCAAATGGCACCTTCAGCAA | 540 |
| 1 | M E P N G T F S N | 9 |
| 541 | TAACAACAGCAGGAACTGCACAATTGAAAACTTCAAGAGAGAATTTTTCCCAATTGTATA | 600 |
| 10 | N N S R N C T I E N F K R E <u>F F P I V Y</u> | 29 |
| 601 | TCTGATAATATTTTTCTGGGGAGTCTTGGGAAATGGGTTGTCCATATATGTTTTCTGCA | 660 |
| 30 | <u>L I I F F W G V L G N G L S I Y V F L Q</u> | 49 |
| 661 | GCCTTATAAGAAGTCCACATCTGTGAACGTTTTTCATGCTAAATCTGGCCATTTTCAGATCT | 720 |
| 50 | P Y K K S T S V N <u>V F M L N L A I S D L</u> | 69 |
| 721 | CCTGTTTATAAGCAGCTTCCCTTCAGGGCTGACTATTATCTTAGAGGCTCCAATTGGAT | 780 |
| 70 | <u>L F I S T L P F R A D Y Y L</u> R G S N W I | 89 |
| 781 | ATTTGGAGACCTGGCCTGCAGGATTATGTCTTATTCCTTGTATGTCAACATGTACAGCAG | 840 |
| 90 | F G D L A C R I M S Y S L Y <u>V N M Y S S</u> | 109 |
| 841 | TATTTATTTCTGACCGTGTGAGTGTGTGCGTTTCTGGCAATGGTTACCCCTTTTCG | 900 |
| 110 | <u>I Y F L T V L S V V R F L A M V</u> H P F R | 129 |

Figure 1B

901 GCTTCTGCATGTCACCAGCATCAGGAGTGCCTGGATCCTCTGTGGGATCATATGGATCCT 960
 130 L L H V T S I R S A W I L C G I I W I L 149

 961 TATCATGGCTTCCTCAATAATGCTCCTGGACAGTGGCTCTGAGCAGAACGGCAGTGTCAC 1020
 150 I M A S S I M L L D S G S E Q N G S V T 169

 1021 ATCATGCTTAGAGCTGAATCTCTATAAAATTGCTAAGCTGCAGACCATGAACTATATTGC 1080
 170 S C L E L N L Y K I A K L Q T M N Y I A 189

 1081 CTTGGTGGTGGGCTGCCTGCTGCCATTTTTCACACTCAGCATCTGTTATCTGCTGATCAT 1140
 190 L V V G C L L P F F T L S I C Y L L I I 209

 1141 TCGGGTTCTGTTAAAAGTGGAGGTCCCAGAATCGGGGCTGCGGGTTTCTCACAGGAAGGC 1200
 210 R V L L K V E V P E S G L R V S H R K A 229

 1201 ACTGACCACCATCATCATCACCTTGATCATCTTCTTCTGTGTTTCCTGCCCTATCACAC 1260
 230 L T T I I I T L I I F F L C F L P Y H T 249

 1261 ACTGAGGACCGTCCACTTGACGACATGGAAAGTGGGTTTATGCAAAGACAGACTGCATAA 1320
 250 L R T V H L T T W K V G L C K D R L H K 269

 1321 AGCTTTGGTTATCACACTGGCCTTGGCAGCAGCCAATGCCTGCTTCAATCCTCTGCTCTA 1380
 270 A L V I T L A L A A A N A C F N P L L Y 289

 1381 TTACTTTGCTGGGAGAATTTTAAGGACAGACTAAAGTCTGCACTCAGAAAAGGCCATCC 1440
 290 Y F A G E N F K D R L K S A L R K G H P 309

 1441 ACAGAAGGCAAAGACAAAGTGTGTTTTCCCTGTTAGTGTGTGGTTGAGAAAGGAAACAAG 1500
 310 Q K A K T K C V F P V S V W L R K E T R 329

 1501 AGTATAAGGAGCTCTTAGATGAGACCTGTTCTGTATCCTTGTGTCCATCTTCATTCACT 1560
 330 V * 331

 1561 CATAGTCTCCAAATGACTTTGTATTTACATCACTCCCAACAAATGTTGATTCTTAATATT 1620

 1621 TAGTTGACCATTACTTTTGTTAATAAGACCTACTTCAAAAATTTTATTTCAGTGTAACAAA 1680

 1681 AAAAAAAAAAAAAAAAAAAAAAAAAA 1708

Figur 2A

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| | | 1 | | 50 |
| HGPRBMY11 | (1) | -----MSLQPSISVSEMEPN-----TFSNNNSRNCITEN--FK | | |
| HGPRBMY11v1 | (1) | MERKFMSLQPSISVSEMEPN-----TFSNNNSRNCITEN--FK | | |
| P2Y5_CHICK | (1) | -----MVSNCSTEDS--FK | | |
| P2YR_CHICK | (1) | MTEALISAALNGTQPELLAGG-----WAAGNATTKCSLTKTGFQ | | |
| P2YR_MELGA | (1) | MTEALISAALNGTQPELLAGG-----WAAGNASTKCSLTKTGFQ | | |
| P2YR_RAT | (1) | MTEVPWSAVPNGTDAAFLAGLSLWGNSTIASAAVSSSFRCALIKTGFQ | | |
| Q9Y271 | (1) | -----MDET-----NLTVSSATCHDTIDDR | | |
| GPRH_HUMAN | (1) | -----MNGLEVAPP-----LITNFSLATAEQCGQETPEE | | |
| | | 51 | | 100 |
| HGPRBMY11 | (22) | REFFPIVYLTIFFWGVLCNGLSIYVLEQPYKSTSVNVEMENLAISDLLL | | |
| HGPRBMY11v1 | (38) | REFFPIVYLTIFFWGVLCNGLSIYVLEQPYKSTSVNVEMENLAISDLLL | | |
| P2Y5_CHICK | (14) | YTLYGCVFSMVEVLGLIANCVAIYIFITLKVNETTTIYMLNLAISDLLL | | |
| P2YR_CHICK | (40) | FYMLPTVYILVFIIGFLGNSVAIWMFVHMRPWSGISVYMENLALADELY | | |
| P2YR_MELGA | (40) | FYMLPTVYILVFIIGFLGNSVAIWMFVHMRPWSGISVYMENLALADELY | | |
| P2YR_RAT | (51) | FYMLPAVYILVFIIGFLGNSVAIWMFVHMRPWSGISVYMENLALADELY | | |
| Q9Y271 | (23) | NQVYSTLYSMESMVGFEENGFLVYVLTKTZHKKSAFQVYMINLAVADLLC | | |
| GPRH_HUMAN | (31) | NMLEASFYLLDFILALVGNLILALWLFTRDHKSGTPANVEMHMLAVADLSC | | |
| | | 101 | | 150 |
| HGPRBMY11 | (72) | ISTLPPRADYYLRGSNWIFGDLACRTMSYSLVNMYSYIFLTVLSVVR | | |
| HGPRBMY11v1 | (88) | ISTLPPRADYYLRGSNWIFGDLACRTMSYSLVNMYSYIFLTVLSVVR | | |
| P2Y5_CHICK | (64) | VFTLPPRIYIEVVRN-WPFGDVLCISVTLEYINMYGSILFTLCISVDR | | |
| P2YR_CHICK | (90) | VLTLPALIEYYENKTDWIFGDVMCKLQRFIEHVNLYGSILFTLCISVHR | | |
| P2YR_MELGA | (90) | VLTLPALIEYYENKTDWIFGDVMCKLQRFIEHVNLYGSILFTLCISVHR | | |
| P2YR_RAT | (101) | VLTLPALIEYYENKTDWIFGDVMCKLQRFIEHVNLYGSILFTLCISAH | | |
| Q9Y271 | (73) | VCTLPPLRVVYVHKGICIMLEGFICRLSTYALYVNLVCSIFEMTAMSFRC | | |
| GPRH_HUMAN | (81) | VLVLPTRIEVYHISGNHWPGEIACRLTGELFYINMYASTIYELTCISADRF | | |
| | | 151 | | 200 |
| HGPRBMY11 | (122) | LAMVHPERLHVTSIRSAILCGTIWILIMASSIMLDS---GSEONGSV | | |
| HGPRBMY11v1 | (138) | LAMVHPERLHVTSIRSAILCGTIWILIMASSIMLDS---GSEONGSV | | |
| P2Y5_CHICK | (113) | LAIVHPERSKTLRTKRNRIVCVAVWITVLAGSTPASEFQSTNRQNNTEQ | | |
| P2YR_CHICK | (140) | TGVVHPKSLGRKKKNNAVYVSSIVWALVAVIAPILEYSGTGVRNRKTI | | |
| P2YR_MELGA | (140) | TGVVHPKSLGRKKKNNAVYVSSIVWALVAVIAPILEYSGTGVRNRKTI | | |
| P2YR_RAT | (151) | SGVVYPKSLGRKKKNNAVYVSVLWLVVVAISEPILEYSGTGIRKNKTV | | |
| Q9Y271 | (123) | IAIVFPQONINLVTKKARFVCGIWIIEVLTSSPELMAKPQKDEKNNIK | | |
| GPRH_HUMAN | (131) | LAIVHPVKSILKRRPLYAHLACAFLLVVVAVAMAPLLVSPQTVQTNHTV | | |
| | | 201 | | 250 |
| HGPRBMY11 | (169) | TSCLE--LNLYKIAKLTQMNYIALVVGCLIPFETLSICYLLIIRVLLKVE | | |
| HGPRBMY11v1 | (185) | TSCLE--LNLYKIAKLTQMNYIALVVGCLIPFETLSICYLLIIRVLLKVE | | |
| P2Y5_CHICK | (163) | RTCFENFPSTWKTYLSRIVIEIEIVGFFIPLINVTGSTMTVLRITLNKPL | | |
| P2YR_CHICK | (190) | TCYDT--TADEYLRSYFVYSMCTTVFMFCIPFIVILGCYGLIVKALITYKD | | |
| P2YR_MELGA | (190) | TCYDT--TADEYLRSYFVYSMCTTVFMFCIPFIVILGCYGLIVKALITYKD | | |
| P2YR_RAT | (201) | TCYDS--TSDEYLRSYFVYSMCTTVAMECIPVLILGCYGLIVRALITYKD | | |
| Q9Y271 | (173) | CFEPP--QDNQTKNHVLYLHYVSLFVGFIIPFVILVVCYTMILITLLKKS | | |
| GPRH_HUMAN | (181) | CLQLY-----REKASHHALVSLAVAFTEPFITTVTCYLLIIRSLRQGL | | |

Figure 2B

| | | | | |
|-------------|-------|------|---|-----|
| | | 251 | | 300 |
| HGPRBMY11 | (217) | VPE | SGLRVSHRKALTTIIITIIFFLCFLPYHTLRTVHL-----TTWKV | |
| HGPRBMY11v1 | (233) | VPE | SGLRVSHRKALTTIIITIIFFLCFLPYHTLRTVHL-----TTWKV | |
| P2Y5_CHICK | (213) | TL | SRNKLS-KKKVLKMFVHIVIFCFQFVPYNITLILYSLMR--TOTWIN | |
| P2YR_CHICK | (238) | LD | NSPLR---RKSTIYLVITVLTVEAVSYLPFHVMKTNLRARLDFOTPO | |
| P2YR_MELGA | (238) | LD | NSPLR---RKSTIYLVITVLTVEAVSYLPFHVMKTNLRARLDFOTPO | |
| P2YR_RAT | (249) | LD | NSPLR---RKSTIYLVITVLTVEAVSYLPFHVMKTNLRARLDFOTPE | |
| Q9Y271 | (221) | MK | NLSS--HKKAIGMTIVVTAALVVSFMPYHIQRTIHLHFLHN--ETKP | |
| GPRH_HUMAN | (224) | RVE | KRLK---TKAVRMIAVLALFLVCFVPYHVNRSVVVLHYR--SHGAS | |
| | | 301 | | 350 |
| HGPRBMY11 | (261) | GL | CKDRHKALVITLALAAANACFNPLLYYFAGENFKDRLKSALRKGHPO | |
| HGPRBMY11v1 | (277) | GL | CKDRHKALVITLALAAANACFNPLLYYFAGENFKDRLKSALRKGHPO | |
| P2Y5_CHICK | (260) | CS | VVTAVRTMYPVTLCTAVSNCCFDPIVYYFTSDTINSELDK--KQQ--VH | |
| P2YR_CHICK | (285) | CAF | NDKVYATYQVTRGLASLNSCVDPILYFLAGDTFRRRLSRATRKSSRR | |
| P2YR_MELGA | (285) | CAF | NDKVYATYQVTRGLASLNSCVDPILYFLAGDTFRRRLSRATRKSSRR | |
| P2YR_RAT | (296) | CD | FNDRVYATYQVTRGLASLNSCVDPILYFLAGDTFRRRLSRATRKASRR | |
| Q9Y271 | (267) | CD | SVLRMOKSVVITLSLAASNCCFDPLLYFFSCGNFRKRLS-TFRKHSL | |
| GPRH_HUMAN | (269) | CAT | ORITALANRITSCTSLNGALDPIMYFFVAEKFRHALCNLLCGKRLK | |
| | | 351 | | 379 |
| HGPRBMY11 | (311) | KAK | -TKCVFPVSVWLRKETRV----- | |
| HGPRBMY11v1 | (327) | KAK | -TKCVFPVSVWLRKETRV----- | |
| P2Y5_CHICK | (306) | QNT | ----- | |
| P2YR_CHICK | (335) | SEP | -NVQSKSEEMTNILTEYKQNGDTSL | |
| P2YR_MELGA | (335) | SEP | -NVQSKSEEMTNILTEYKQNGDTSL | |
| P2YR_RAT | (346) | SEA | -NLQSKSEEMTNILSEFKQNGDTSL | |
| Q9Y271 | (316) | SVT | -YVPRKASLPEKGEEICKV----- | |
| GPRH_HUMAN | (319) | GPPP | SEEGKTNESSLSAKSEL----- | |

Figure 3

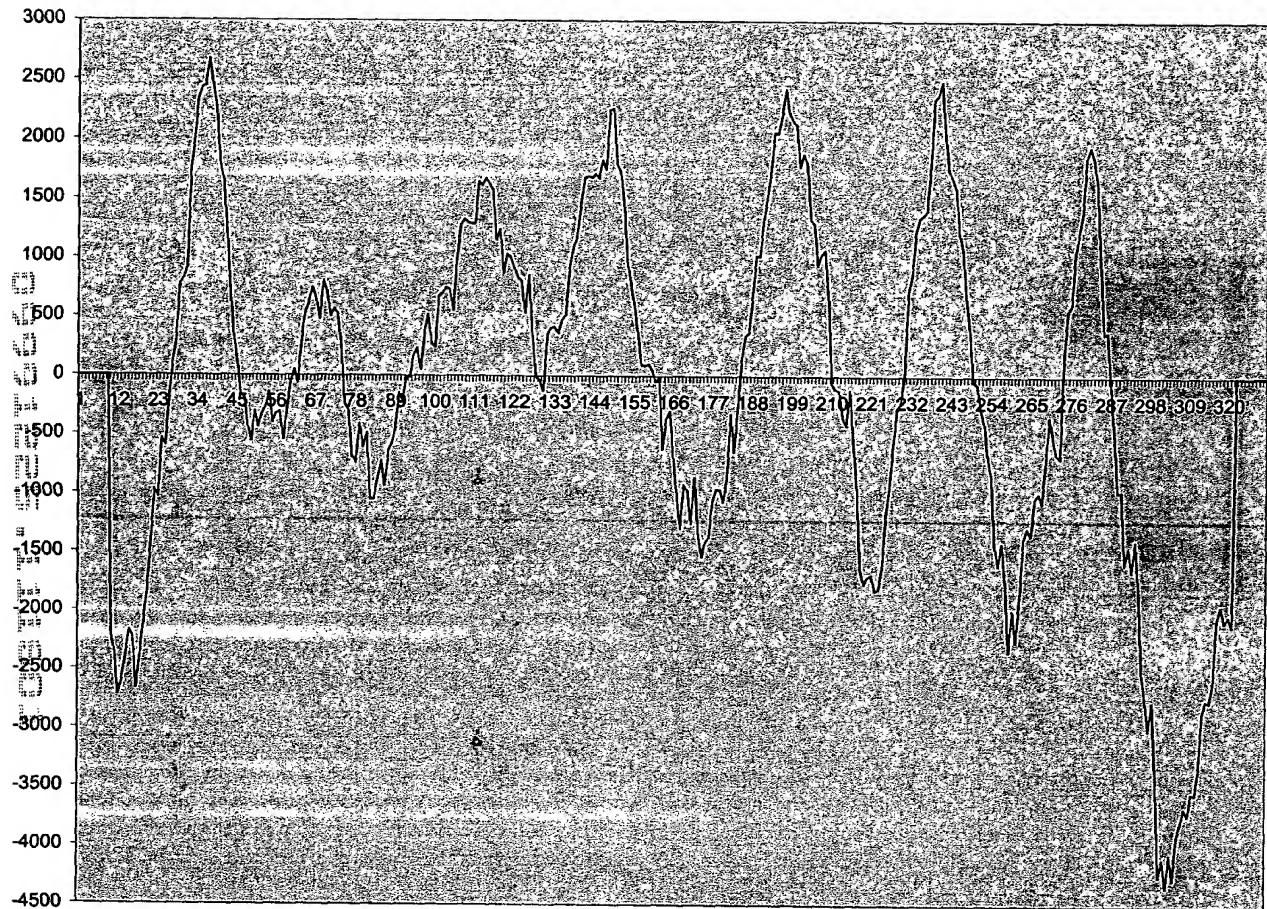


Figure 4.

Expression Profiling of Novel Human GPCR, HGPRBMY11

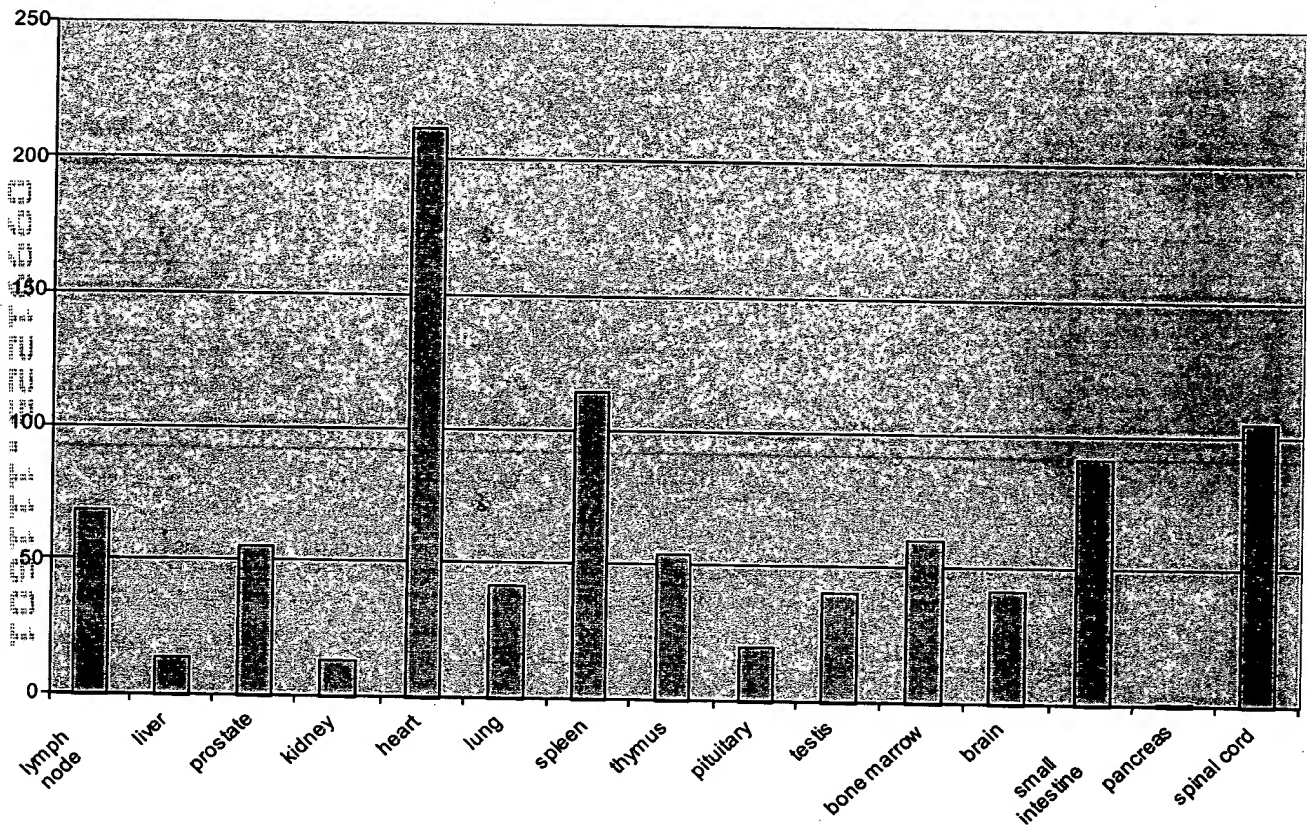


Figure 5.

HGPRBMY11

| Protein | Genbank ID | Identities | Similarities |
|--|-------------------|-------------------|---------------------|
| human cysteinyl leukotriene receptor | gi 11422069 | 37% | 49% |
| chick purinergic receptor 5 | gi P32250 | 36% | 46% |
| human G-protein-coupled receptor GPR17 | gi Q13304 | 36% | 46% |
| chick purinergic receptor | gi P34996 | 30% | 45% |
| turkey purinergic receptor | gi P49652 | 30% | 45% |
| rat purinergic receptor | gi P49651 | 30% | 44% |

HGPRBMY11v1

| Protein | Genbank ID | Identities | Similarities |
|--|-------------------|-------------------|---------------------|
| human cysteinyl leukotriene receptor | gi 11422069 | 37.2% | 49% |
| chick purinergic receptor 5 | gi P32250 | 36.7% | 46.1% |
| human G-protein-coupled receptor GPR17 | gi Q13304 | 36.2% | 46.1% |
| chick purinergic receptor | gi P34996 | 29.5% | 43.9% |
| turkey purinergic receptor | gi P49652 | 29.8% | 44.2% |
| rat purinergic receptor | gi P49651 | 29.6% | 44% |

Figure 6A

1 ATGGAGAGAAAAATTTATGTCTTGCAACCATCCATCTCCGTATCAGAAATGGAACCAAAT 60
 1 M E R K F M S L Q P S I S V S E M E P N 20

 61 GGCACCTTCAGCAATAACAACAGCAGGAAGTGCACAATTGAAAACCTCAAGAGAGAATTT 120
 21 G T F S N N N S R N C T I E N F K R E F 40

 121 TTCCCAATTGTATATCTGATAATATTTTCTGGGGAGTCTTGGGAAATGGGTTGTCCATA 180
 41 F P I V Y L I I F F W G V L G N G L S I 60

 181 TATGTTTTCTGCAGCCTTATAAGAAGTCCACATCTGTGAACGTTTTTCATGCTAAATCTG 240
 61 Y V F L Q P Y K K S T S V N V F M L N L 80

 241 GCCATTTTCAGATCTCCTGTTTATAAGCACGCTTCCCTTCAGGGCTGACTATTATCTTAGA 300
 81 A I S D L L F I S T L P F R A D Y Y L R 100

 301 GGCTCCAATTGGATATTTGGAGACCTGGCCTGCAGGATTATGTCTTATTCCTTGTATGTC 360
 101 G S N W I F G D L A C R I M S Y S L Y V 120

 361 AACATGTACAGCAGTATTTATTTCTGACCGTGCTGAGTGTGTGCGTTTTCTGGCAATG 420
 121 N M Y S S I Y F L T V L S V V R F L A M 140

 421 GTTCACCCCCTTCGGCTTCTGCATGTCACCAGCATCAGGAGTGCTGGATCCTCTGTGGG 480
 141 V H P F R L L H V T S I R S A W I L C G 160

 481 ATCATATGGATCCTTATCATGGCTTCTCAATAATGCTCCTGGACAGTGGCTCTGAGCAG 540
 161 I I W I L I M A S S I M L L D S G S E Q 180

 541 AACGGCAGTGTACATCATGCTTAGAGCTGAATCTCTATAAAATTGCTAAGCTGCAGACC 600
 181 N G S V T S C L E L N L Y K I A K L Q T 200

 601 ATGAACTATATTGCCTTGGTGGTGGGCTGCCTGCTGCCATTTTTCACACTCAGCATCTGT 660
 201 M N Y I A L V V G C L L P F F T L S I C 220

 661 TATCTGCTGATCATTCGGGTCTGTGTTAAAGTGGAGGTCCCAGAATCGGGGCTGCGGGTT 720
 221 Y L L I I R V L L K V E V P E S G L R V 240

 721 TCTCACAGGAAGGCACTGACCACCATCATCATCACCTTGATCATCTTCTTCTGTGTTTC 780
 241 S H R K A L T T I I I T L I I F F L C F 260

 781 CTGCCCTATCACACACTGAGGACCGTCCACTTGACGACATGGAAAGTGGGTTTATGCAAA 840
 261 L P Y H T L R T V H L T T W K V G L C K 280

 841 GACAGACTGCATAAAGCTTTGGTTATCACACTGGCCTTGGCAGCAGCCAATGCCTGCTTC 900
 281 D R L H K A L V I T L A L A A A N A C F 300

Figure 6B

901 AATCCTCTGCTCTATTACTTTGCTGGGGAGAATTTTAAGGACAGACTAAAGTCTGCACTC 960
301 N P L L Y Y F A G E N F K D R L K S A L 320

961 AGAAAAGGCCATCCACAGAAGGCAAAGACAAAGTGTGTTTTCCCTGTTAGTGTGTGGTTG 1020
321 R K G H P Q K A K T K C V F P V S V W L 340

1021 AGAAAAGGAAACAAGAGTATAA 1041
341 R K E T R V 346

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Figure 7

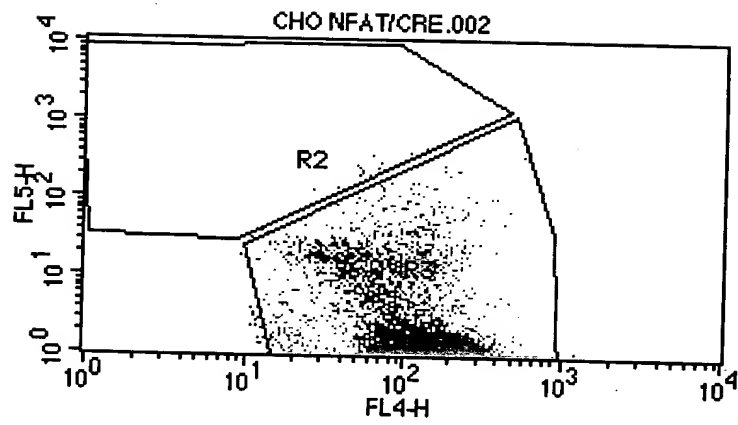


Figure 9

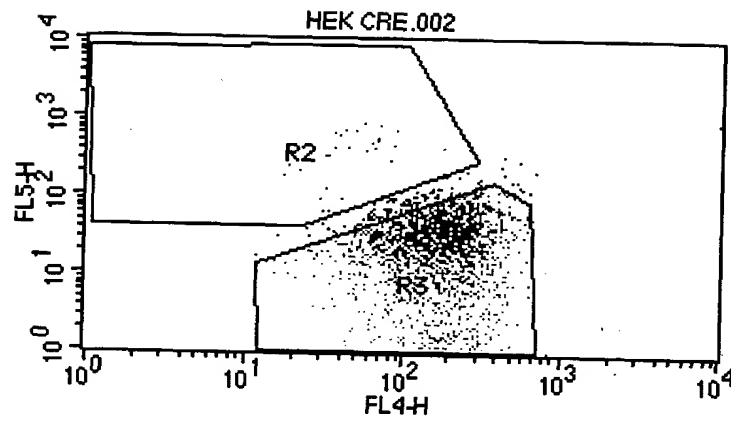


Figure 10

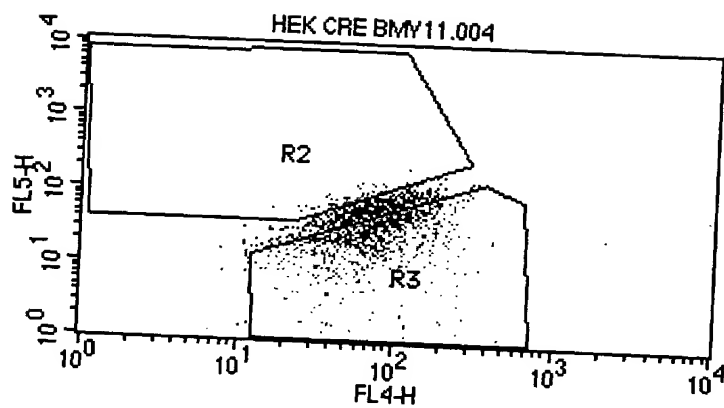


Figure 11

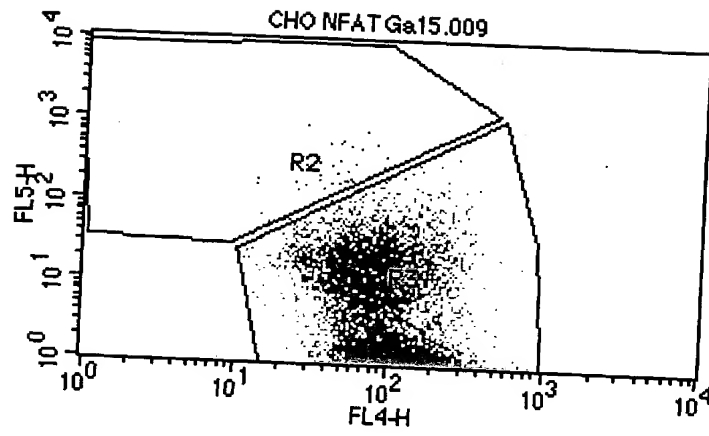


Figure 12

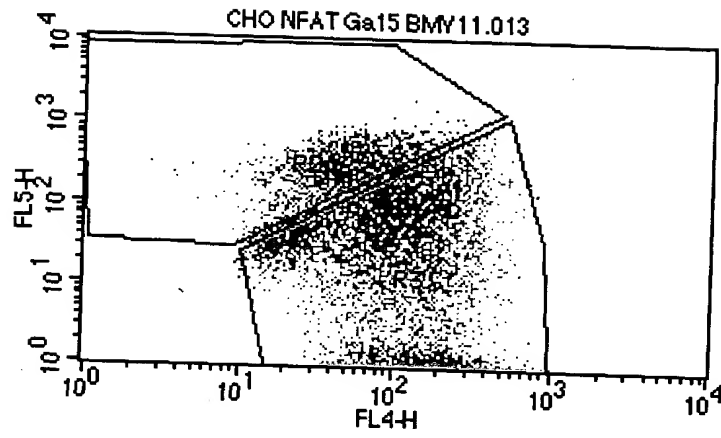
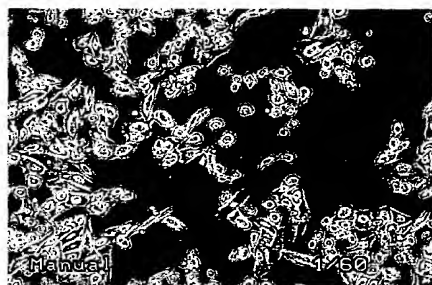
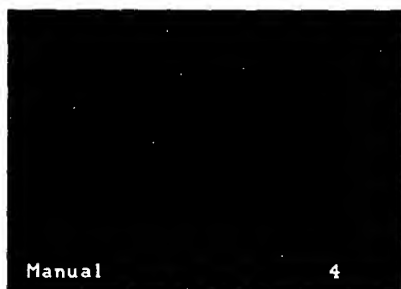


Figure 13

Cho NFAT Gal5 Control (Fluorescent vs. Bright Field)



Cho NFAT Gal5 BMY11 (Fluorescent vs. Bright Field)

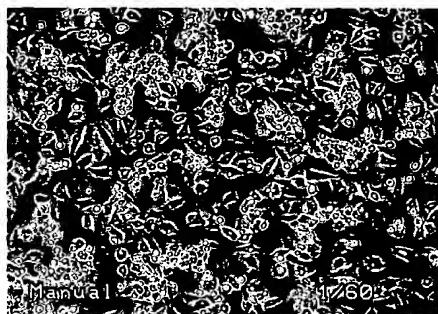
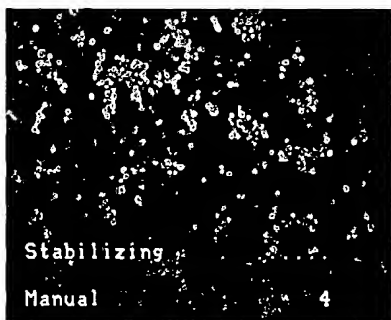
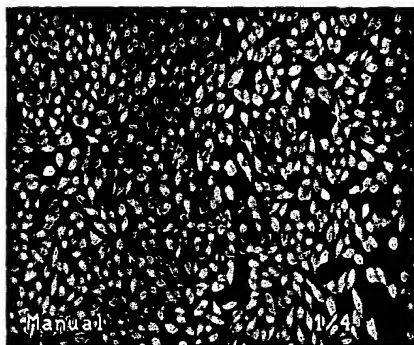
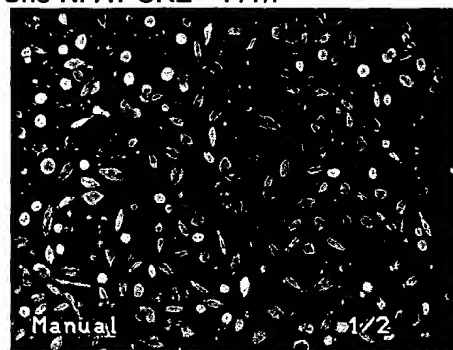


Figure 14

a. Cho-NFAT CRE



b. Cho-NFAT CRE + F/T/P



c. Cho-NFAT CRE oGPCR-Intermediate



d. Cho-NFAT CRE oGPCR High

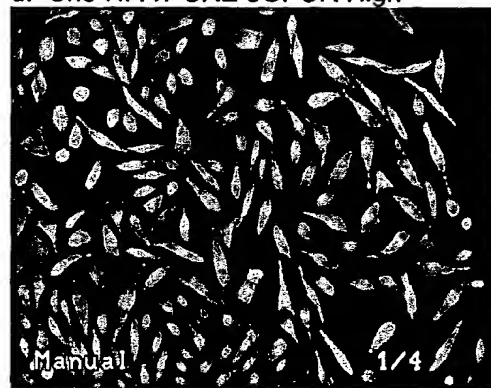


Figure 15A

1 ATGTCCTTGCAACCATCCATCTCCGTATCAGAAATGGAACCAAATGGCACCTTCAGCAAT 60
 1 M S L Q P S I S V S E M E P N G T F S N 20

 61 AACAAACAGCAGGAACTGCACAATTGAAAACCTCAAGAGAGAATTTTTCCCAATTGTATAT 120
 21 N N S R N C T I E N F K R E F F P I V Y 40

 121 CTGATAATATTTTTCTGGGGAGTCTTGGGAAATGGGTTGTCCATATATGTTTTCTGCAG 180
 41 L I I F F W G V L G N G L S I Y V F L Q 60

 181 CCTTATAAGAAGTCCACATCTGTGAACGTTTTTCATGCTAAATCTGGCCATTTTCAGATCTC 240
 61 P Y K K S T S V N V F M L N L A I S D L 80

 241 CTGTTTCATAAGCACGCTTCCCTTCAGGGCTGACTATTATCTTAGAGGCTCCAATTGGATA 300
 81 L F I S T L P F R A D Y Y L R G S N W I 100

 301 TTTGGAGACCTGGCCTGCAGGATTATGTCTTATTCCTTGTATGTCAACATGTACAGCAGT 360
 101 F G D L A C R I M S Y S L Y V N M Y S S 120

 361 ATTTATTTCTGACCGTGCTGAGTGTGTGCGTTTCCTGGCAATGGTTCCACCCCTTTTCGG 420
 121 I Y F L T V L S V V R F L A M V H P F R 140

 421 CTTCTGCATGTCACCAGCATCAGGAGTGCCTGGATCCTCTGTGGGATCATATGGATCCTT 480
 141 L L H V T S I R S A W I L C G I I W I L 160

 481 ATCATGGCTTCCTCAATAATGCTCCTGGACAGTGGCTCTGAGCAGAACGGCAGTGTCA 540
 161 I M A S S I M L L D S G S E Q N G S V T 180

 541 TCATGCTTAGAGCTGAATCTCTATAAAATTGCTAAGCTGCAGACCATGAACTATATTGCC 600
 181 S C L E L N L Y K I A K L Q T M N Y I A 200

 601 TTGGTGGTGGGCTGCCTGCTGCCATTTTTACACTCAGCATCTGTTATCTGCTGATCATT 660
 201 L V V G C L L P F F T L S I C Y L L I I 220

 661 CGGGTTCTGTAAAGTGGAGGTCCCAGAATCGGGGCTGCGGGTTTCTCACAGGAAGGCA 720
 221 R V L L K V E V P E S G L R V S H R K A 240

 721 CTGACCACCATCATCATCACCTTGATCATCTTCTTCTTGTTTCTGCTGCTGATCATT 780
 241 L T T I I I T L I I F F L C F L P Y H T 260

 781 CTGAGGACCGTCCACTTGACGACATGGAAAGTGGGTTTATGCAAAGACAGACTGCATAAA 840
 261 L R T V H L T T W K V G L C K D R L H K 280

 841 GCTTTGGTTATCACACTGGCCTTGGCAGCAGCCAATGCCTGCTTCAATCCTCTGCTCTAT 900
 281 A L V I T L A L A A A N A C F N P L L Y 300

Figure 15B

901 TACTTTGCTGGGGAGAATTTTAAGGACAGACTAAAGTCTGCACTCAGAAAAGGCCATCCA 960
301 Y F A G E N F K D R L K S A L R K G H P 320

961 CAGAAGGCAAAGACAAAGTGTGTTTTCCCTGTTAGTGTGTGGTTGAGAAAGGAAACAAGA 1020
321 Q K A K T K C V F P V S V W L R K E T R 340

1021 GTATAA 1026
341 V 341

1021 GTATAA 1026
341 V 341